
Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2009; month=12; day=3; hr=14; min=4; sec=20; ms=455;]

Validated By CRFValidator v 1.0.3

Application No: 10590034 Version No: 3.0

Input Set:

Output Set:

Started: 2009-11-09 23:46:09.574

Finished: 2009-11-09 23:46:09.976

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 402 ms

Total Warnings: 4

Total Errors: 0

No. of SeqIDs Defined: 6

Actual SeqID Count: 6

Error code		Error Description									
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(3)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(4)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(5)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEO	ID	(6)

SEQUENCE LISTING

<110>	Genomine, Inc. Korea Research Institute of Chemical Technology	
<120>	Polypeptide Participating in Pyridoxine Biosynthesis, a Polynucleotide Coding the Polypeptide and Those Uses	
<130>	DJKIM.GENO.PT1	
<140>		
<141>	2009-11-09	
	PCT/KR05/000453 2006-08-18	
	PCT/KR2005/000453 2005-02-18	
<150> <151>		
<160>	6	
<170>	PatentIn version 3.5	
<210>	1	
<211>	1297	
<212> <213>		
\Z13>	Arabidopsis charrana	
<400>	1	
tcactat	taaa gccgatccat agataaacga ggaccggcca gaaatcgctt caccattccc	60
aaatct	ctct tccattttct ccacacaaat ttctcttcaa tctccgataa tggaaggaac	120
cggcgtt	tgtg gcggtgtacg gtaacggtgc gataacggag gcgaagaaat ctcccttctc	180
cgtgaaq	ggtc ggtttggctc agatgctccg tggtggtgtt atcatggatg tcgtcaacgc	240
cgagca	aget egtategeeg aggaggetgg tgettgegee gteatggett tggagegtgt	300
tcctgct	tgat atccgcgctc aaggaggcgt cgctcgtatg agcgatccac aaatgattaa	360
agaaat	caaa caagccgtta cgattccggt gatggctaag gctaggattg gtcatttcgt	420
tgaagct	tcag atccttgaag caattggaat cgattacatc gatgagagcg aggttttgac	480
tcttgct	tgat gaagatcatc acatcaacaa gcataatttc cggatcccgt tcgtttgcgg	540
ttgccg	gaat ctcggcgagg ctctgaggag gatccgtgaa ggtgcggcga tgattaggac	600
caaaggt	tgaa gctggaaccg gtaacattat tgaagctgtg aggcatgtga ggtctgttaa	660
tggtgad	catt agggttttgc gaaacatgga tgatgatgag gttttcactt tcgctaagaa	720
attagco	cgct ccgtacgatc tcgtgatgca gactaagcag cttggtcgtc ttcctgtagt	780

ccaattcgcc	gccggtggag	tggctactcc	ggctgatgca	gctctcatga	tgcagcttgg	840
atgtgatggt	gtctttgttg	gttctggtat	cttcaagagc	ggtgacccag	ctcgtcgtgc	900
acgtgccatt	gttcaggctg	tgactcatta	cagtgaccct	gagatgcttg	tggaggtgag	960
ctgtgggctt	ggagaagcca	tggttgggat	caatctcaac	gatgagaagg	ttgagaggtt	1020
cgctaatcgc	tccgagtgat	caaagaaata	aaaggtaaaa	tatctcagac	gaaatggttt	1080
cagaattttc	tcagaccatt	ttgcagtaat	ctctttgaaa	agaagaagat	gatgatattg	1140
ttggtagttt	gtatcctttg	tgttttcctt	ataatctttg	atagtctttt	gttattgtaa	1200
ctcgtaatcc	ctttgcaaga	acaagtttgt	cagttataat	aatgtactac	tctcttgatc	1260
gatcagttgg	ttttgaatct	gatatattct	tcgatcc			1297

<210> 2

<211> 309

<212> PRT

<213> Arabidopsis thaliana

<400> 2

Met Glu Gly Thr Gly Val Val Ala Val Tyr Gly Asn Gly Ala Ile Thr 1 5 10 15

Glu Ala Lys Lys Ser Pro Phe Ser Val Lys Val Gly Leu Ala Gln Met 20 25 30

Leu Arg Gly Gly Val Ile Met Asp Val Val Asn Ala Glu Gln Ala Arg 35 40 45

Ile Ala Glu Glu Ala Gly Ala Cys Ala Val Met Ala Leu Glu Arg Val 50 55 60

Pro Ala Asp Ile Arg Ala Gln Gly Gly Val Ala Arg Met Ser Asp Pro 65 70 75 80

Gln Met Ile Lys Glu Ile Lys Gln Ala Val Thr Ile Pro Val Met Ala 85 90 95

Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln Ile Leu Glu Ala Ile 100 105 110

Gly Ile Asp Tyr Ile Asp Glu Ser Glu Val Leu Thr Leu Ala Asp Glu 115 120 125

Asp His His Ile Asn Lys His Asn Phe Arg Ile Pro Phe Val Cys Gly 135 140 Cys Arg Asn Leu Gly Glu Ala Leu Arg Arg Ile Arg Glu Gly Ala Ala 150 155 145 160 Met Ile Arg Thr Lys Gly Glu Ala Gly Thr Gly Asn Ile Ile Glu Ala 165 170 175 Val Arg His Val Arg Ser Val Asn Gly Asp Ile Arg Val Leu Arg Asn 180 185 Met Asp Asp Glu Val Phe Thr Phe Ala Lys Lys Leu Ala Ala Pro 200 195 Tyr Asp Leu Val Met Gln Thr Lys Gln Leu Gly Arg Leu Pro Val Val 210 215 220 Gln Phe Ala Ala Gly Gly Val Ala Thr Pro Ala Asp Ala Ala Leu Met 230 225 235 240 Met Gln Leu Gly Cys Asp Gly Val Phe Val Gly Ser Gly Ile Phe Lys 250 2.45 Ser Gly Asp Pro Ala Arg Ala Arg Ala Ile Val Gln Ala Val Thr 260 265 270

His Tyr Ser Asp Pro Glu Met Leu Val Glu Val Ser Cys Gly Leu Gly 275 280

Glu Ala Met Val Gly Ile Asn Leu Asn Asp Glu Lys Val Glu Arg Phe 295 300 290

Ala Asn Arg Ser Glu 305

<210> 3 <211> 30 <212> DNA <213> Artificial Sequence

<223> Sense Primer

<220>

<400>	3					
gaagat	ctat ggaaggaacc ggcgttgtgg	30				
<210>	4					
<211>	32					
<212>	DNA					
<213>	Artificial Sequence					
<220>						
<223>	Antisense Primer					
<400>	4					
cgaagct	tttt ataactgaca aacttgttct tg	32				
<210>	5					
<211>						
	DNA					
<213>	Artificial Sequence					
<220>						
	Sense Primer					
\223/	sense Filmer					
<400>	5					
	ctca ctcggagcga ttagcgaac	29				
gaagae	ocou ocoyyayoya coayoyaao					
<210>	6					
<211>	30					
<212>	DNA					
<213>	Artificial Sequence					
<220>						
<223>	Antisense primer					
<400>	6					
gctctag	getetagatg gaaggaaceg gegttgtgge 30					